sequence is FHGGSWYRFPWGY-NH2, corresponding to a calculated average mass of 1659.8 Da (Average mass observed in ESI MS = 1659.3 Da).

Change(s) applied to document, /T.M.C./ 1/4/2012

In the paragraph from page 6, line 31 to page 7, line 9:

Confirmation of the determined sequence was achieved by two independent methods. First, a synthetic peptide corresponding to the determined sequence of Mo1659 was prepared and its MS/MS fragmentation pattern shown to be identical to that of the natural product ~~(Figure 5)~~. The identity of the synthetic and natural peptides was also established by HPLC analysis ~~(Figure 5, inset)~~. Second, conventional Edman sequencing using an automated sequenator confirmed the sequence. A notable feature of Mo1659 is the presence of as many as seven aromatic amino acids (F-2, Y-2, W-2, H-1) in a short stretch of 13 residues. The positively charged peptide is notably deficient in the common aliphatic, hydrophobic amino acids like Ala, Val, Leu and Ile.

In the paragraph on page 9, lines 8-25:

Mo1659 shows K+ channel modulating activity in DRG neurons. ~~Figure 6 shows the effect of Mo1659 on the mixed whole-cell outward K+ currents from a DRG neuron.~~ A marked reduction in the current amplitudes at all the potentials was observed with 200 nM of the Mo1659 in the external bath solution. The mixed K+ currents have a fast transient current and a sustained current component. The fast transient current component was dissected from the sustained current component using two different pre- pulse voltages followed by identical voltage protocols ~~that are shown schematically in Figure 7~~. Although the K+ current components cannot be fully isolated using the conditioning prepulse voltages alone (18), the results suggest that Mo1659 addition to the external bath solution predominantly affects the sustained K+ current component. It may be noted that the transient current component, that was obtained following subtraction of current traces, is not significantly affected by Mo1659. Similar results were obtained in 5 different experiments. Mo1659 thus appears to affect non-inactivating voltage dependent potassium channels. The reduction of total K+ currents in excitable cells by blocking potassium channels is a process, which is important in developing therapeutics for arrhythmias and heart failure. Enhancing the duration of action potentials using potassium channel blockers is a possible strategy for the development of new classes of antiarrhythmic agents.

AMENDMENTS TO THE SPECIFICATION

Please amend the specification as follows:

Change(s) applied to document, /T.M.C./ 1/4/2012

In the paragraph from page 3, line 25 to page 4, line 24:

The specimen, *Conus monile* was collected from the southeast coast of India. The venom ducts after dissection were preserved in ethanol and the venom that oozes out was subjected to High Performance Liquid Chromatography (HPLC) purification after concentration on a rotavapor. Crude venom extract was applied onto a Jupiter 4μ, Proteo 90Å, C_{18} column (10 mm x 250 mm) and eluted with a linear gradient of acetonitrile containing 0.1% TFA. The flow rate was maintained at 1ml min^{-1} and the absorbance was monitored at 226 nm. Fractionation into several peptide components was achieved. The peptide components were analyzed by MALDI mass spectra analysis of individual HPLC fractions. The intense component at the retention time of 23.4 minutes corresponding to a molecular mass of 1659 Da was chosen for mass spectrometric de_novo sequencing. The peptide component showed a high resolution MALDI mass spectrum, which establishes [M+H]+ = 1659.1 Da (monoisotopic mass). ~~The inset shows the charge states observed in an electrospray mass spectrum, where the~~ The +2 and +3 states are detectable suggesting the presence of at least three protonatable groups in the molecule. Attempted reduction with DTT followed by alkylation with iodoacetamide left the molecular mass unchanged, establishing the *absence* of disulfide bonds. Acetylation with acetic anhydride and acetic acid yielded a product with a mass [M+H]+ = 1701.3 Da (Δm = +42Da) indicating the presence of a single primary amino group. UV and fluorescence spectra established the presence of both Trp and Tyr residues. Peptide sequencing was undertaken using MALDI MS/MS techniques selecting the 1659.1 Da as the precursor ion. ~~Figure 3 shows the observed fragment ions along with assignments of the b and y ion series (13).~~ The presence of an intense b2 ion at 285 Da permitted sequential tracing of the 8-residue segment –GGSWYRFP-. The immonium ions at 70, 110, 136 and 159 suggested the presence of the residues Pro, His, Tyr and Trp, respectively. The b2 ion at 285 Da could correspond to the dipeptide –FH- or –HF- at the amino terminus. The observation of mass peaks at 194.9 Da suggested the presence of the dipeptide ion –GH- or –HG-. This supports the assignment of the sequence –FHG- at the N-terminus. The